

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/973,451
DATE: 12/04/2001
TIME: 20:18:50

Input Set : N:\Crf3\RULE60\09973451.raw
Output Set: N:\CRF3\12042001\I973451.raw

PS

ENTERED

1 <110> APPLICANT: JACOBSON, Myron K.
2 JACOBSON, Elaine L.
3 AM, Jean-Christophe
4 LIN, Winston
5 <120> TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE
6 (PARG) ENZYMES,
7 THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE
8 THEREWITH
9 <130> FILE REFERENCE: NIAD 201
10 <140> CURRENT APPLICATION NUMBER: 09/973,451
11 <141> CURRENT FILING DATE: 2001-10-09
12 <150> PRIOR APPLICATION NUMBER: US/09/302,812
13 <151> PRIOR FILING DATE: 1999-04-30
14 <150> PRIOR APPLICATION NUMBER: 60/083,768
15 <151> PRIOR FILING DATE: 1998-05-01
16 <160> NUMBER OF SEQ ID NOS: 38
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19 <211> LENGTH: 4070
20 <212> TYPE: DNA
21 <213> ORGANISM: Bos taurus
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26 ctgcagaagc agtcagcggc agagggggca tgggtgccggg aggcaccgag gagggggcgc 180
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28 gtgctgcggg tcccagcatg agtgcggggc cgggctgtga gccctgcacc aagcgacccc 300
29 gctgggacgc cgctgcaact tctccgccgg ccgcctcgga cgcccgagc ttccccggca 360
30 ggcagaggcg cgtcctcgat tccaaggacg ctccgggtgca gttcagggtc ccgccgtcct 420
31 cgtcaggctg cgccctgggc cgggcggggac agcaccgagg cagcgccacc tctcttgttt 480
32 tcaaacagaa gactataacc agttggatgg aactaaagg aatcaagaca gttgaatcag 540
33 aaagtgttga tagtaaagaa aacaacaata caagagaaga atccatgatg agttctgtac 600
34 aaaaagataa cttttatcaa cataacatgg aaaaattaga aaatgtttct cagctagggt 660
35 ttgataagtc accagttgaa aaaggtacac agtatttgaa gcagcatcag actgcggcta 720
36 tgtgtaagtg gcagaatgaa gggccacact cagaacggct tttggaaagt gaacctccag 780
37 cggtaactct ggtaccagag cagttcagta atgctaattg cgatcagtcg tccccaaagg 840
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39 taaagcttgc gaatgcaaag cagacgatgg aagatgaaca gggcagagaa gccagaagcc 960
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41 agacagacgt ggtgtccgag agccccttgt cggacactgg ctctgaggat gttggtactg 1080
42 gactgaaaaa tgccaacaga ttgaatagac aagaaagtag tctaggaaat tctcctccat 1140
43 ttgagaaaga aagtgaacct gagtcaccaa tggatgtaga taattccaaa aatagttgtc 1200
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51      ttggaactcc tattgaggag atgaggagaa tgccaagggtg tgggatccgg ctgcctccct 1680
52      tgagaccatc tgccaatcac acagtgacta ttcgggtaga tcttttgcga ataggagaag 1740
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93 <210> SEQ ID NO: 2

94 <211> LENGTH: 977

95 <212> TYPE: PRT

96 <213> ORGANISM: Bos taurus

97 <220> FEATURE:

98 <400> SEQUENCE: 2

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99      Met Ser Ala Gly Pro Gly Cys Glu Pro Cys Thr Lys Arg Pro Arg Trp
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101      Asp Ala Ala Ala Thr Ser Pro Pro Ala Ala Ser Asp Ala Arg Ser Phe
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103      Pro Gly Arg Gln Arg Arg Val Leu Asp Ser Lys Asp Ala Pro Val Gln
104          35          40          45
105      Phe Arg Val Pro Pro Ser Ser Ser Gly Cys Ala Leu Gly Arg Ala Gly
106          50          55          60
107      Gln His Arg Gly Ser Ala Thr Ser Leu Val Phe Lys Gln Lys Thr Ile
108      65          70          75          80
109      Thr Ser Trp Met Asp Thr Lys Gly Ile Lys Thr Val Glu Ser Glu Ser
110          85          90          95
111      Leu His Ser Lys Glu Asn Asn Asn Thr Arg Glu Glu Ser Met Met Ser
112          100          105          110
113      Ser Val Gln Lys Asp Asn Phe Tyr Gln His Asn Met Glu Lys Leu Glu
114          115          120          125
115      Asn Val Ser Gln Leu Gly Phe Asp Lys Ser Pro Val Glu Lys Gly Thr
116          130          135          140
117      Gln Tyr Leu Lys Gln His Gln Thr Ala Ala Met Cys Lys Trp Gln Asn
118      145          150          155          160
119      Glu Gly Pro His Ser Glu Arg Leu Leu Glu Ser Glu Pro Pro Ala Val
120          165          170          175
121      Thr Leu Val Pro Glu Gln Phe Ser Asn Ala Asn Val Asp Gln Ser Ser
122          180          185          190
123      Pro Lys Asp Asp His Ser Asp Thr Asn Ser Glu Glu Ser Arg Asp Asn
124          195          200          205
125      Gln Gln Phe Leu Thr His Val Lys Leu Ala Asn Ala Lys Gln Thr Met
126          210          215          220
127      Glu Asp Glu Gln Gly Arg Glu Ala Arg Ser His Gln Lys Cys Gly Lys
128      225          230          235          240
129      Ala Cys His Pro Ala Glu Ala Cys Ala Gly Cys Gln Gln Glu Glu Thr
130          245          250          255
131      Asp Val Val Ser Glu Ser Pro Leu Ser Asp Thr Gly Ser Glu Asp Val
132          260          265          270
133      Gly Thr Gly Leu Lys Asn Ala Asn Arg Leu Asn Arg Gln Glu Ser Ser
134          275          280          285
135      Leu Gly Asn Ser Pro Pro Phe Glu Lys Glu Ser Glu Pro Glu Ser Pro
136          290          295          300
137      Met Asp Val Asp Asn Ser Lys Asn Ser Cys Gln Asp Ser Glu Ala Asp
138      305          310          315          320
139      Glu Glu Thr Ser Pro Gly Phe Asp Glu Gln Glu Asp Ser Ser Ser Ala
140          325          330          335
141      Gln Thr Ala Asn Lys Pro Ser Arg Phe Gln Pro Arg Glu Ala Asp Thr
142          340          345          350
143      Glu Leu Arg Lys Arg Ser Ser Ala Lys Gly Gly Glu Ile Arg Leu His
144          355          360          365
145      Phe Gln Phe Glu Gly Gly Glu Ser Arg Ala Gly Met Asn Asp Val Asn
146          370          375          380
147      Ala Lys Arg Pro Gly Ser Thr Ser Ser Leu Asn Val Glu Cys Arg Asn

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148	385		390		395		400
149	Ser Lys Gln His Gly Arg Lys Asp Ser Lys Ile Thr Asp His Phe Met						
150		405		410		415	
151	Arg Val Pro Lys Ala Glu Asp Lys Arg Lys Glu Gln Cys Glu Met Lys						
152		420		425		430	
153	His Gln Arg Thr Glu Arg Lys Ile Pro Lys Tyr Ile Pro Pro His Leu						
154		435		440		445	
155	Ser Pro Asp Lys Lys Trp Leu Gly Thr Pro Ile Glu Glu Met Arg Arg						
156		450		455		460	
157	Met Pro Arg Cys Gly Ile Arg Leu Pro Pro Leu Arg Pro Ser Ala Asn						
158		465		470		475	
159	His Thr Val Thr Ile Arg Val Asp Leu Leu Arg Ile Gly Glu Val Pro						
160		485		490		495	
161	Lys Pro Phe Pro Thr His Phe Lys Asp Leu Trp Asp Asn Lys His Val						
162		500		505		510	
163	Lys Met Pro Cys Ser Glu Gln Asn Leu Tyr Pro Val Glu Asp Glu Asn						
164		515		520		525	
165	Gly Glu Arg Ala Ala Gly Ser Arg Trp Glu Leu Ile Gln Thr Ala Leu						
166		530		535		540	
167	Leu Asn Arg Leu Thr Arg Pro Gln Asn Leu Lys Asp Ala Ile Leu Lys						
168		545		550		555	
169	Tyr Asn Val Ala Tyr Ser Lys Lys Trp Asp Phe Thr Ala Leu Ile Asp						
170		565		570		575	
171	Phe Trp Asp Lys Val Leu Glu Glu Ala Glu Ala Gln His Leu Tyr Gln						
172		580		585		590	
173	Ser Ile Leu Pro Asp Met Val Lys Ile Ala Leu Cys Leu Pro Asn Ile						
174		595		600		605	
175	Cys Thr Gln Pro Ile Pro Leu Leu Lys Gln Lys Met Asn His Ser Ile						
176		610		615		620	
177	Thr Met Ser Gln Glu Gln Ile Ala Ser Leu Leu Ala Asn Ala Phe Phe						
178		625		630		635	
179	Cys Thr Phe Pro Arg Arg Asn Ala Lys Met Lys Ser Glu Tyr Ser Ser						
180		645		650		655	
181	Tyr Pro Asp Ile Asn Phe Asn Arg Leu Phe Glu Gly Arg Ser Ser Arg						
182		660		665		670	
183	Lys Pro Glu Lys Leu Lys Thr Leu Phe Cys Tyr Phe Arg Arg Val Thr						
184		675		680		685	
185	Glu Lys Lys Pro Thr Gly Leu Val Thr Phe Thr Arg Gln Ser Leu Glu						
186		690		695		700	
187	Asp Phe Pro Glu Trp Glu Arg Cys Glu Lys Leu Leu Thr Arg Leu His						
188		705		710		715	
189	Val Thr Tyr Glu Gly Thr Ile Glu Gly Asn Gly Gln Gly Met Leu Gln						
190		725		730		735	
191	Val Asp Phe Ala Asn Arg Phe Val Gly Gly Gly Val Thr Ser Ala Gly						
192		740		745		750	
193	Leu Val Gln Glu Glu Ile Arg Phe Leu Ile Asn Pro Glu Leu Ile Val						
194		755		760		765	
195	Ser Arg Leu Phe Thr Glu Val Leu Asp His Asn Glu Cys Leu Ile Ile						
196		770		775		780	

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199   Arg Trp Ala Arg Ser His Glu Asp Arg Ser Glu Arg Asp Asp Trp Gln
200                               805                               810                               815
201   Arg Arg Thr Thr Glu Ile Val Ala Ile Asp Ala Leu His Phe Arg Arg
202                               820                               825                               830
203   Tyr Leu Asp Gln Phe Val Pro Glu Lys Ile Arg Arg Glu Leu Asn Lys
204                               835                               840                               845
205   Ala Tyr Cys Gly Phe Leu Arg Pro Gly Val Ser Ser Glu Asn Leu Ser
206                               850                               855                               860
207   Ala Val Ala Thr Gly Asn Trp Gly Cys Gly Ala Phe Gly Gly Asp Ala
208   865                               870                               875                               880
209   Arg Leu Lys Ala Leu Ile Gln Ile Leu Ala Ala Ala Val Ala Glu Arg
210                               885                               890                               895
211   Asp Val Val Tyr Phe Thr Phe Gly Asp Ser Glu Leu Met Arg Asp Ile
212                               900                               905                               910
213   Tyr Ser Met His Thr Phe Leu Thr Glu Arg Lys Leu Thr Val Gly Glu
214                               915                               920                               925
215   Val Tyr Lys Leu Leu Leu Arg Tyr Tyr Asn Glu Glu Cys Arg Asn Cys
216                               930                               935                               940
217   Ser Thr Pro Gly Pro Asp Ile Lys Leu Tyr Pro Phe Ile Tyr His Ala
218   945                               950                               955                               960
219   Val Glu Ser Cys Thr Gln Thr Thr Asn Gln Pro Gly Gln Arg Thr Gly
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224 <211> LENGTH: 4069
225 <212> TYPE: DNA
226 <213> ORGANISM: Homo sapiens
227 <220> FEATURE:
228 <400> SEQUENCE: 3
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231   gctctccgcg gggccggccc ggggacagtg cgctgctggt cccagcatga atgcgggccc 180
232   cggctgtgaa ccctgcacca aagcgacccg ctggggcgcc gctacaactt cgccggctgc 240
233   ttcggacgcc cggagctttc cgagcaggca gaggcgcgtc ctcgacccca aggacgctca 300
234   cgtgcagttc agggteccac cgtcctcgcc agcctgcgtc ccagggcagg cgggacagca 360
235   cagaggcagc gccacctcgc ttgttttcaa acaaaagact attaccagtt ggatggacac 420
236   taaaggaatc aagacagcgg aatcagaaag tttggatagt aaagaaaaca acaatacaag 480
237   aatagaatcc atgatgagtt ctgtacaaaa agataacttt taccaacata atgtagaaaa 540
238   attagtaaat gtttctcagc taagtcttga taagtcactc actgaaaaaa gtacacagta 600
239   tttgaaccag catcagactg cagcaatgtg taagtggcaa aatgaaggga aacacacgga 660
240   gcagcttttg gaaagtgaac ctcaaacagt aacctggta ccagagcagt ttagtaatgc 720
241   taacattgat cggtcacctc aaaatgatga tcacagtgc acagatagtg aagagaatag 780
242   agacaatcaa cagtttctca caactgtaaa gcttgcaaat gcaaagcaga ctacggaaga 840
243   tgaacacgcc agagaagcca aaagccacca gaagtgcagc aagtcttgcc atcctgggga 900
244   agactgtgca agttgtcagc aagatgagat agacgtggtg ccaaagagtc cattgtcaga 960
245   tgttggctct gaggatgttg gtactgggtc aaaaaatgac aacaaattga ttagacaaga 1020
246   aagttgccta ggaaattctc ctccatttga gaaggaaagt gaaccogaat caccgatgga 1080

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : N:\Cr3\RULE60\09973451.raw

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L:946 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:946 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:946 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:946 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:964 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
L:964 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:964 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14
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L:981 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1165 M:256 W: Invalid Numeric Header Field, <220> has non-blank data